

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

Figure 1

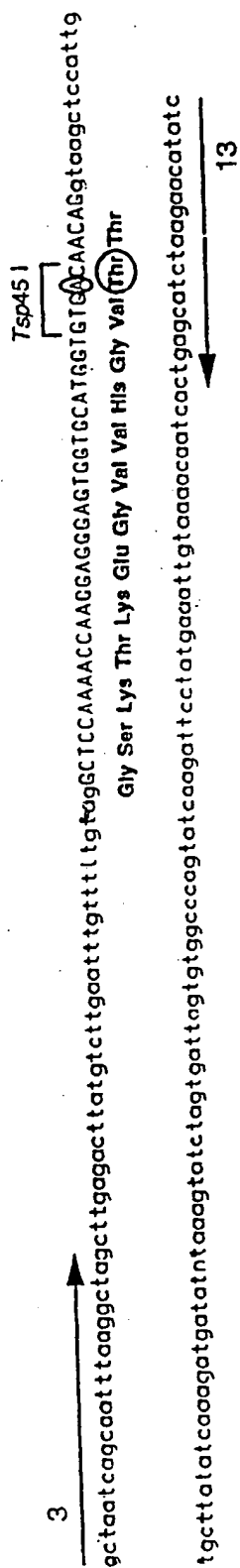


Figure 2

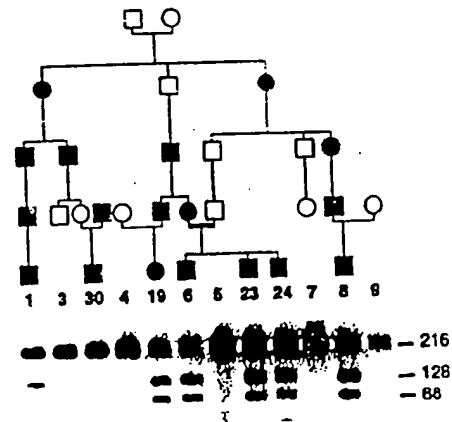


Figure 3

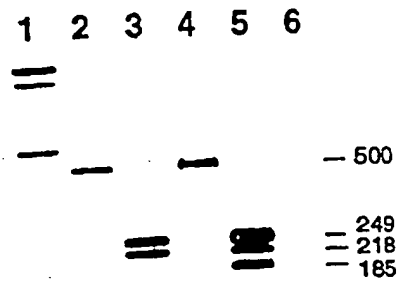


Figure 4

1	MDVFMKGLSKAKKEGVVAAAEKTKQGVAAEAAAGKT	30	1	KEGVLY	Homo sapiens
1	MDVFMKGLSKAKKEGVVAAAEKTKQGVAAEAAAGKT	20	1	KEGVLY	Rattus norvegicus
1	MDVFMKGLSKAKKEGVVAAAEKTKQGVAAEAAAGKT	10	1	KEGVLY	Bos taurus
1	MDVFMKGLSKAKKEGVVAAAEKTKQGVAAEAAAGKT	1	1	KEGVLY	Serinus canaria
1	MDVFMKGLSKAKKEGVVAAAEKTKQGVAAEAAAGKT	1	1	KEGVLY	Torpedo californica
40	VGSKTKKEGVVHGVVATVAAEKTKEQVTVNVGGAVVTGVTAVAQKTV	60	1	EGAGSIA	Homo sapiens
40	VGSKTKKEGVVHGVVATVAAEKTKEQVTVNVGGAVVTGVTAVAQKTV	50	1	EGAGSIA	Rattus norvegicus
40	VGSKTKKEGVVHGVVATVAAEKTKEQVTVNVGGAVVTGVTAVAQKTV	40	1	EGAGSIA	Bos taurus
40	VGSKTKKEGVVHGVVATVAAEKTKEQVTVNVGGAVVTGVTAVAQKTV	30	1	EGAGSIA	Serinus canaria
51	VGTKTKEGVVQSVNTVTETKEQANVVGGAVVAGVNTVASKTV	20	1	EGVENV	Torpedo californica
90	AATGFFVKKDDQLGK-N--EEGAPQ--EGI--LED--MPVDPDNEAYEMPS	100	1	EMPS	Homo sapiens
90	AATGFFVKKDDQMGK-G--EEGYPPQ--EGI--LED--MPVDPDNEAYEMPS	90	1	EMPS	Rattus norvegicus
79	AATGLVKKEEFPT-DLKPVEEVAQ--EAAEEPLIE--PLMEPEGESEYEEQP	80	1	EEQP	Bos taurus
90	AATGLVKKDDQLAKQN--EEGFLLQ--EGM--VNNTGAADVDPDNEAYEMPP	70	1	EMPP	Serinus canaria
101	AASGVVKKLDEHGR-EIPAEQVAEBGKQTTQEPLVB--ATEATE--	60	1	EMPP	Torpedo californica
130	EEGYQDDYEPEA	50	1	EMPP	Homo sapiens
130	EEGYQDDYEPEA	40	1	EMPP	Rattus norvegicus
124	QEEYQEEYEPEA	30	1	EMPP	Bos taurus
133	EEYQDDYEPEA	20	1	EMPP	Serinus canaria
140	EEYQDDYEPEA	10	1	EMPP	Torpedo californica
	ETGK	1	1	EMPP	

Figure 5

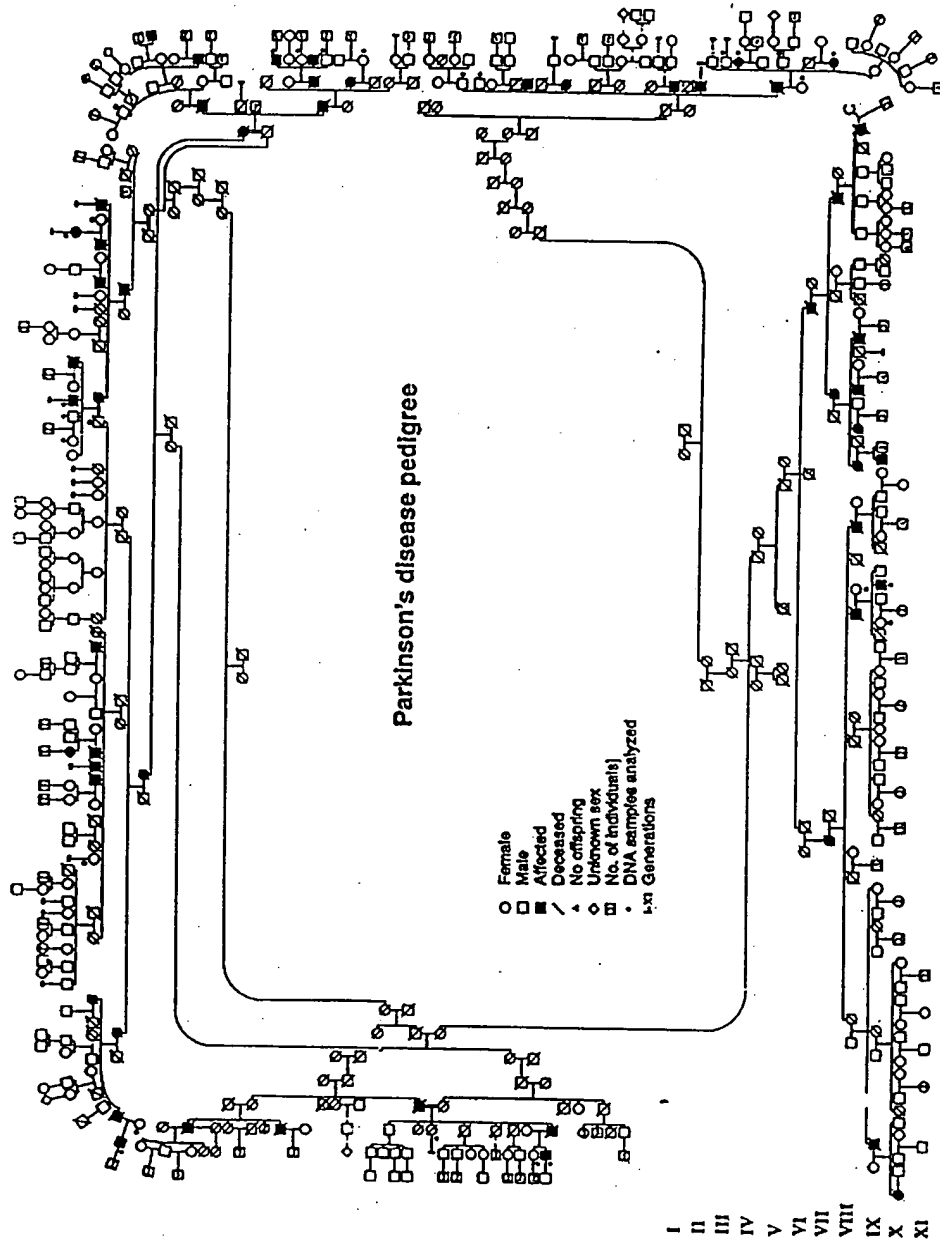


Figure 6

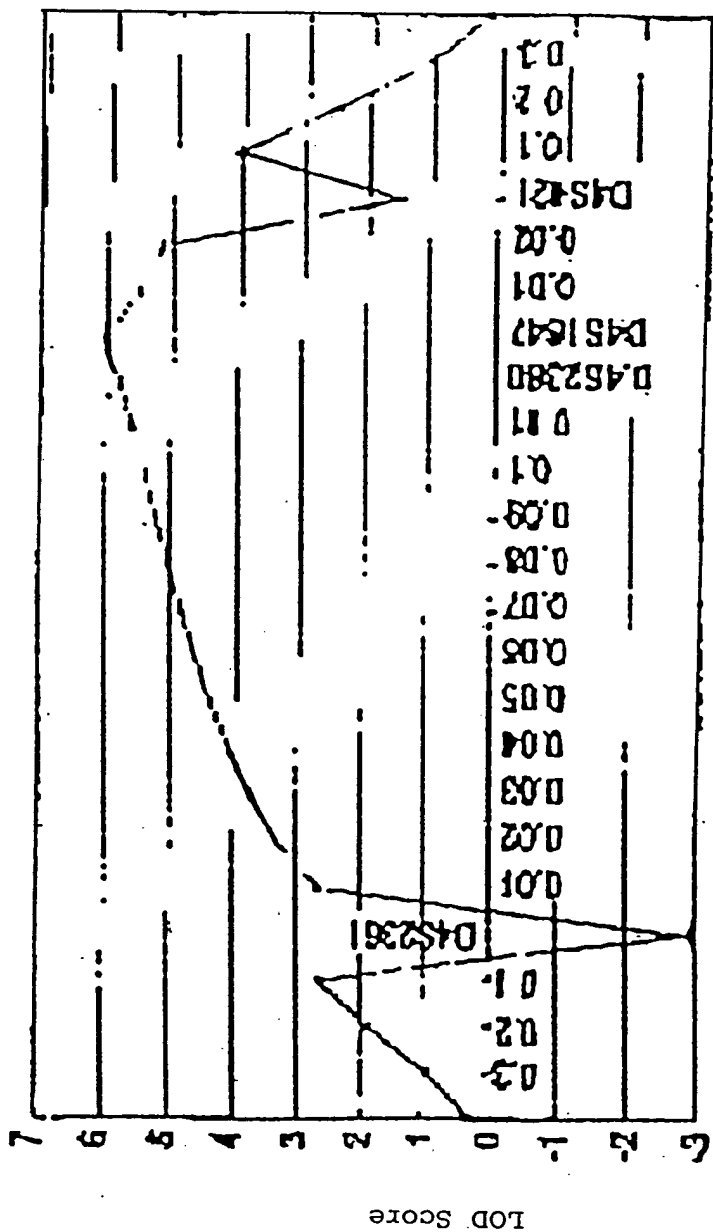


Figure 7

clone	5'	3'	gene
109979	T84229	T88834	alpha
111088	T83410		alpha
111090	T83411	T81593	alpha
130048	R11619	(R19409)	alpha
135534	R31354	R32856	alpha
141248	R66863	R67383	alpha
145594	R78091	R77746	alpha
171906	H19290	H19291	beta
172284	H19556	H19474	beta
172749		H19685	beta
176546		H41126	beta
193174	H47503	H47504	alpha
210768	H66914	H66869	alpha
213616	H70324	H70325	alpha
236027	H62070		alpha
248153	N53829	N73325	alpha
24991	(T80528)	R39000	alpha
26298	R13508	(R20629)	alpha
265817	N28661	N21457	alpha
286628		N22757	alpha
27342		R37173	alpha
280344	(N50305)	N47094	alpha
290894		N72005	alpha
294142		N68597	alpha
307787	W21278		alpha
340635	W56712	W56757	alpha
340683	W55988	W56278	alpha
346647	W94390	W74638	alpha
346796	W79585	W79784	alpha
359349	AA010546	AA010547	alpha
364632	AA022809	AA022690	alpha
39915		R50455	beta
40764	R56327	R56245	alpha
45086	H08908	H08824	alpha
46807	H10267	H10213	alpha
49811	H29080	H28976	alpha
50202		H17962	beta
50470		H16811	beta
66473	R16018	R16119	alpha
667794	AA258686	AA258608	alpha
69907	T48654	T48655	alpha
72381	AA394097	AA293803	gamma
739009	AA421586		beta
739014	(AA42185)	AA421567	beta
771303		AA443638	gamma
2-4		L36675	alpha
2-5		L36874	alpha
c-01f08		F01363	alpha
c-1rb08	F03254	F06981	alpha
c-2td12	F08836	F11169	alpha
c-28f08	F03751	F07521	alpha
cDNA	S69965		beta
EST01420 (HRBAA27)	M78265		gamma
EST19193	AA317129		beta
EST22040	AA319774		alpha

Figure 7 cont.

EST26845	T28079		beta
EST31489	AA328063		alpha
EST68G11	W22518		gamma
F1-825D	R29481		alpha
GEN-129D09	D81090		beta
hbc590	T11070		alpha
HIBBA65	T08213	T08212	alpha
	HR70E3R	HR70E3F	alpha
HSNACP0		U46896-46901	alpha
KK1311	N83633		alpha
		D318839	alpha
		L08850	alpha
	T28735		alpha
	Z20502		alpha

Figure 8

10 20 30 40 50 60 70
 CCGCGCCAGCCGCGCTCCATCCCCAGCCCGGCCCGCATCCGGTTTGGAGGGGGCTGCAAGTTTGCA 70
 AGGGGCCCCGGGAXAAAAAXCGAGCAGTGGCCCTTCCCGCGTCCCCAGGGTTTCAAGGGACGCTAGGAXTX 140
 TCCGCGGCCCTGGAGGTTTCGCACTGGGGAGTGGGGTGAGATGGGGGAAAGCGGGAGGGGGCTCAGGGTC 210
 CAGAAGGGCXCXCGGGTCTCGGGAGTAGGGGGGCATXTCGCTCCCGGGAGGGGCTGGGGTGAGAGTGC 280
 GGGGCCAGTGCACCGGTGCCCGTATCGCCCTCCCCAGGCCGCCAGGATGGACGTGTTTCATGAAGGGCC 350
 360 370 380 390 400 410 420
 TGTCCATGGCCAAGGAGGGCGTTGTGGCAGCCGCGGAGAAAACCAAGCAGGGGGTACCGAGGGCGGGGA 420
 GAAGACCAAGGAGGGCGTCTCTACGTGGGTGGGCGXGGGGCGGGTTTCTGGGGCTGCAGGGCTGGGGG 490
 TCCCCCTACAGTGTGGAGCTGGGGCCGGGTCCCGGGGAGGGGGGTTCTGGGCAAGATAATATXAXTCAGC 560
 AGATGGGGCXAGGTCAAXXGGGTCTAAGGGACATACCCAXCCCATAGAAXCCTGGGTCTGTATCCGGA 630
 AATGGGGACACGGGGCGGGCTGATGAGGTGGGGGGCTCCAXCTGAAAGGCCAGGGACCAXTGCAXTXATA 700
 710 720 730 740 750 760 770
 AAAXCACACAXCCTCTTTTCTTATCTTTTTTACCATTATTAATAGTTATCTGGTGTGAACACTTTCT 770
 GTATGCCAAGTACTGGGTAAATGTCTAATCATCCATTCTCATGTAATGCTTCCGCCCATTTCTACAGG 840
 TAAGGGAACTGGGCTTCCCATTTGGTAGXTAAATTTTAGGTTTCAAGAGGCTTGAATTGAATGTCAGTTC 910
 AGCCAATTTCTTAGTGGTGAACCAAACTGAGTTCCATCCGTGAAACGGGGACAATAACAGCACCCGCTT 980
 CCCAGGGCTGGGGAAAAGTGAAGTGCAGCGGGGAGGACAGGACTTGACACAGCACTGGCCCTCAGCCA 1050
 1060 1070 1080 1090 1100 1110 1120
 ACATCCACTAGAGGGGTGGGGTATCGCATCAGGTGGGAGAGAACTGCAACCCCTGCAGACAGAGGTGTGG 1120
 GGCCCACTGAGTGATAAGACGGGGTTAACATGGGGGTGCAGGTTGTAGGATXGGGGACCAAGGAGG 1190
 CAGTGACGGGGCCAGGATGCCACTCTGTAAATCACCATGCTGTGCTGGAGTTTCTGTTCCCTCAGCGCAG 1260
 AGTCTTAAATGTGCGCTTTTCTXCCCIGCAGGAAGCAAGACCCGAGAAAGGTGTGGTACAAGGTGTGG 1330
 CITCAGGTACTAGCCAGCCCTGGCACCAGCCCTTCTCTCAHTTAGGCGGATGATCTGGCCGGGAACCAG 1400
 1410 1420 1430 1440 1450 1460 1470
 AGGGCGGGGGCGGGGAGACTCCCAAGGCTTCTGCGGGAATGCTCCGTGGGGAGGGCAGGCCCTGGGATA 1470
 CTACAAGGCAGGGCATCGGTGTTTCCCCCTGGCTCCCAACCCCTTCTCAACCCCTCCCTGCTCCAGT 1540
 GGCTGAAAAAACCAAGGAACAGGCCCTCACATCTGGGAGGAGCTGTGTTCTCTGGGGCAGGGAACATCGCA 1610
 GCAGCCACAGGACTGGTGAAGAGGGAGGAATTCCTACTGATCTGAAGGTAAAGCATCCTTCTGACCCGC 1680
 ACATGCAAGCAAC 1750
 1760 1770 1780 1790 1800 1810 1820
 CCCCCCTAATCCTGCCACCAGCTTGGAAACACAAGCCACTTTGCCTCCCATCTGCXGGCCCGTGCTAGAC 1820
 TCAGCTCAGAATGCATCTGAATAAXGGCGTGCATGGGTGTGACGCTCCCGGTGATGGGGACCCAGACCTG 1890
 GCTGTCTCGGTGTATCCTGCTTGCCAGCGTGACCCATATGACTTCTGGCCACGTCTGCATGTGTCAATGA 1960
 TTGTTTATTCTTTTCTTTTCAACAAATATCCATGCCAXXCCAGCCCTGTCTTGAAGTTCCAGXT 2030
 CCCTTTAGCCXAGGGGAGCXTGAGGGTTATTTTGGGGTCCCGATGCCAGCACAGAGCCTGACACAAA 2100
 2110 2120 2130 2140 2150 2160 2170
 GGATGAGGCATAAGCTGGTGAGTATCCAAATGGTGAAGTGTGGAGGXTGCCAGGCATTGGGGGAG 2170
 CGGCGTGGAGAGCCAGCTCCCAATCCATGCTGCCACTTCAACTGTGATTGCGGGGAATTTCCCCCTTCA 2240
 CCTCCATCCCACTTCCAAGGCACTCCAAATAAATAACTGAATTAGAAATTATCCTTGTGTTTGCACCCCA 2310
 CCCTAGCCTTCCCACTCCAACCCACCCAAAGCTTACCACTGTGGGAATTTGGGGGGCATCCTGGCTGTC 2380
 CTCACGAGTCTGACCTTTCTGCCACAGCCAGAGGAAGTGGCCAGGAAGCTGCTGAAGAACCCTGA 2450
 2460 2470 2480 2490 2500 2510 2520
 TTGAGCCCCGTGATGGAGCCAGAAGGGGAGAGTTATGAGGACCCACCCAGGAGGAATATCAGGAGTATGA 2520
 GCCAGAGGCGTAGGGGCCAGGAGAGCCCCACAGCAGCACAAATCTGTCCCTGTCCCTGCCCCGCCCC 2590
 CCAGAGCCAGGGCTGTCTTAGACTCCTTCTCCCCAATCAGAGATCTTCTTCCGCTCTGAGGCAACCC 2660
 CCTCGAGCCTGTGTAGTGTCTGTCCATCTGTCTGTCTACCCGCCCCGCTCAACCCCGGGGCATGGA 2730
 CAGGGCCAGGGTTGCGGTGCGGGCTGGGAGCCTCGCCCTCCAGTGTGCTCTCCATCCAGCGTCTG 2800
 2810 2820 2830 2840 2850 2860 2870
 CGCG 2804

Figure 9

```

      10      20      30      40
      |      |      |      |
AGGGAGATCCAGCTCCGTCCTGCCTGCAGCAGCACAAACC 40
TGCACACCCACCATGGATGTCTTCAAGAAGGGCTTCTCCA 80
TCGCCAAGGAGGGXGTGGTGGGTGCGGTGGAAAAGACCAA 120
GCAGGGGGTGACGGAAGCAGCTGAGAAGACCAAGGAGGGG 160
GTCATGTATGTGGGATTACATTTTTTTTTTAAAGAAAGAA 200
      210      220      230      240
      |      |      |      |
TAAATTAATTGTGATTAAAGTTG 223

```

Figure 10

```

      10      20      30      40
      |      |      |      |
TTTTTXXAGGGGGGAAAACAGGGAATAXAAAAAXXGXXX 40
GGGGGTTTTTXXGGGGGGGGGGGAAAAXGGTTXGGGGGX 80
XAACCXAAAXAAAXCCXAXGGGGGGGGXXAXTXAAXTTT 120
TGGGAACCCAAAGCCCXAGGAGGATTTTTXGTXAAXAACG 160
TXACCTCXAGTGGGXCGAGGAAGACCAAGGAAAXGCCCAA 200
      210      220      230      240
      |      |      |      |
CXCGTTGAXCGAGGCTGTGGTGAACAXCGTXCAACXCTG 240
TGCCXCCAAXAXCGTGGAGGXGGGGGAGAACATCSCGGT 280
CACCTCCGGGGTGGTGGCGMAGGAGGACTTGAGGCCATCT 320
KCCCCCMACAGGAGGGTGTGGCATCCMAAGARAAAGAGG 360
AAGTGGCAGAGGAGGCCAGAGTGGGGGARACTAGAGGGC 400
      410      420      430      440
      |      |      |      |
TACAGGCCAGCGTGGATGACCTGAAGAGCGCTCCTCTGCC 440
TTGGACACCATCCCCTCCTAGCACAAAGGAGTGCCCGCCTT 480
GAGTGACATGCGGCTGCCCACGCTCCTGCCCTCGTCTTCC 520
TGGCCACCCTTGGCCTGTCCACCTGTGCTGCTGCACCAAC 560
CTCACTGCCCTCCCTCGGCCCCACCCACCCTCTGGTCCTT 600
      610      620      630      640
      |      |      |      |
CTGACCCCACTTATGCTGCTGTGAATTTTTTTTTTAAATG 640
ATTECAAATAAACTTGAGCCCACTCCAAAAAATAA 677

```

Figure 11

alpha-SYN exons 1-2

```

      10      20      30      40
      |      |      |      |
AATTT CAGCG ATGCG AGGGCAA AGCGCTCTCGGCGGTGCG 40
GTGTG AGCCACCTCCCGGCGCTGCCTGTCTCCTCCAGCAG 80
CTCCCCAAGGGATAGGCTCTGCCCTTGGTGGTCGACCCCTC 120
AGGCCCTCGNTCTCCAGGNCGACTCTGACGAGGGGTAGG 160
GGGTGGTCCCNNGAGGACCCAGAGGAAAGGCNNGGACAA 200

      210      220      230      240
      |      |      |      |
GAAGGGAGGGGAAGGGGAAAGAGGAAGAGGCATCATCCCT 240
AGCCCAACCGCTCCCGATCTCCACAAGAGTGCTCGTGACC 280
CTAAACTTAACGTGAGGCGCAAAGCGCCCCAACCTTTTC 320
CCGCCTTGNNCCAGGCAGGCGGCTGGAGTTGATGGCTCAC 360
CCGCGCCCCCTGCCCATCCCCATCCGAGATAGGGACGA 400

      410      420      430      440
      |      |      |      |
GGAGCACGCTGCAGGGAAAGCAGCGAGCGCCGGGAGAGGG 440
GCGGGCAGAAGCGCTGACAAATCAGCGGTGGGGGCGGAGA 480
GCCGAGGAGAAGGAGAAGGAGGAGGACTAGGAGGAGGAGG 520
ACGGCGACGACCAGAAGGGGCCCAAGAGAGGGGGCGAGCG 560
ACCGAGCGCCGCGACGCGAAGTGAGGTGCGTGCGGGCTCA 600

      610      620      630      640
      |      |      |      |
GCGCAGACCCCGGCCCGGCCCTCCTGAGAGCGTCCTGGG 640
CGCTCCCTCACGCCTTGCTTCAAGCCTTCTGCCTTTCCA 680
CCCTCGTGAGCGGAGAACTGGGAGTGGCCATTCGACGACA 720
GGTTAGCGGGTTTGCTTCCACTCCCCCAGCCTCGCGTCG 760
CCGGCTCACAGCGGCCTCTCTGGGGACAGTCCCCCCCCGG 800

      810      820      830      840
      |      |      |      |
GTGCCCCCTCCGCCCTTCTGTGCGCTCCTTTTCTTCTTC 840
TTTCCTATTAAATATTATTGGGAATTGTTAAATTTTTT 880
TTTTAAAAAAGAGAGAGGCGNGGAGGAGTCGGAGTTGTG 920
GAGAAGCAGAGGGACTCAGGTAAGTACCTGTGGATCTAAA 960
CGGNGTCTTTGGAAATCCTGGAGAACGCCGGATGGAGAC 1000

      1010      1020      1030      1040
      |      |      |      |
GAATGGTCGTGGGNACCGGGAGGGGTGGTGCTGCCATGA 1040
GGACCGCTGGGCCAGGTCTCTGGGAGGTGAGTACTTGTCC 1080
TTTGGGGAGCCTAAGGAAAGAGACTTGACCTGGCTTTTCGT 1120
CCTGCTTCTGATATTCCTTCTCCACAAGGGCTGAGAGNT 1160
TAGGCTGCTTCTCCGGGATCC 1181

```

Figure 11 cont.

alpha-SYN exon 3

```
      10      20      30      40
+-----+
CTTAAAAGAGTCTCACACTTTGGAGGGTTTCTCATGATTT 40
TTCAGTGTTTTTGTATTTTTCCCGAAAAGTTCTCATT 80
CAAAGTGATTTTATGTTTTCCAGTGTTGTAAAGAAAT 120
TCATTAGCCATGGATGTATTCATGAAAGGACTTTCAAAGG 160
CCAAGGAGGGAGTTGTGGCTGCTGCTGAGAAAACCAAACA 200
      210      220      230      240
+-----+
GGGTGTGGCAGAAGCAGCAGGAAAGACAAAAGAGGGTGTT 240
CTCTATGTAGGTAGGTAAACCCCAAATGTCAGTTTGGTGC 280
TTGTTTCATGAGTGATGGGTTAGGATAACAATACTCTAAAT 320
GCTGGTAGTTCTCTCTCTTGATTCATTTTTGCATCATTGC 360
TTGTCAAAAAGGTGGACTGAGTCAGAGGTATGTGTAGGTA 400
      410      420      430      440
+-----+
GGTGAATGTGAACGTGTGTATNTGAGCTAATAGTAAAAAT 440
GCGACTGTTTGCTTTTCAGATTTTAAATTTGCCTAATAT 480
NTATGACTTNTTAAAAATGAATGTTTCTGTACTACATAATT 520
CTATNTCAGAGACAGT 536
```

Figure 11 cont.

alpha-SYN exon 4

10 20 30 40
CTGCAGGTCAACGGATCTGTCTCTAGTGCTGTACTTTTAA 40
AGCTTCTACAGTTCTGAATTCAAAATTATCTTCTCACTGG 80
GCCCCGGTGTTATCTCATTCTTTTTCTCCTCTGTAAGTT 120
GACATGTGATGTGGGAACAAAGGGGATAAAGTCATTATTT 160
TGTGCTAAAATCGTAATTGGAGAGGACCTCCTGTTAGCTG 200
210 220 230 240
GGCTTTCTTCTATNTATTGTGGTGGTTAGGAGTTCCTTCT 240
TCTAGTTTTAGGATATATATATATATTTTTTCTTCCCT 280
GAAGATATAATAATATATATACTTCTGAAGATTGAGATTT 320
TTAAATTAGTTGTATTGAAAAGTCTAATCAGCAATTTA 360
AGGCTAGCTTGAGACTTATGTCTTGAATTTGTTTTGTAG 400
410 420 430 440
GCTCCAAAACCAAGGAGGGAGTGGTGCATGGTGTGGCAAC 440
AGGTAAGCTCCATTGTGCTTATATCAAAGATGATATNTAA 480
AGTATCTAGTGATTAGTGTGGCCAGTATCAAGATTCCTA 520
TGAAATTGTAAAACAATCACTGAGCATCTAAGAACATATC 560
AGTCTTATTGAACTGAATTCCTTATAAAGTATTTTTTAA 600
610 620 630 640
TAGGTAAATATTGATTATAAATAAAAAATATACTTGCCAA 640
GAATAATGAG 650

Figure 11 cont.

alpha-SYN exon 5

```
      10      20      30      40
.....|.....|.....|.....|
ATATCTTAGCCAAGATTCAATGTTTGGTTGAACCACACTC 40
ACTTGACATCTTGGTGGCTTTTGTTCCTTCTGACCACTCA 80
GTTATCTATGGCATGTGTAGATACAGGTGTATGGAANCGA 120
TGGCTAGTGGAAGTGGAATGATTTTAAGTCACTGTTATTC 160
TACCACCCTTTAATCTGTTGTTGCTCTTTATTTGTACCAG 200

      210      220      230      240
.....|.....|.....|.....|
TGGCTGAGAAGACCAAAGAGCAAGTGACAAATGTTGGAGG 240
AGCAGTGGTGACGGGTGTGACAGCAGTAGCCCAGAAGACA 280
GTGGAGGGAGCAGGGAGCATTGCAGCAGCCACTGGCTTTG 320
TCAAAAAGGACCAGTTGGGCAAGGTATGGCTGTGTACGTT 360
TTGTGTTACATTTATAAGCTGGTGAGATTACGGTTCATTT 400

      410      420      430      440
.....|.....|.....|.....|
TCATGTGAAGCCTGGAGGCAGGAGCAAGATACTTACTGTG 440
GGGAACGGCTACCTGACCCTCCCCTTGTGAAAAAGTGCTA 480
CCTTTATATTGGTCTTGCTTGTTT 504
```

10 20 30 40
AAAAGTTTACATACTTTGAGGTTGATAACCCATGTTGCCG 40
CAATGTTTCCCCGGAGGCATTGTGGAGTTTAGAATGCCAG 80
TAGTAATATTAAGGTGTGCCATTTTCAAGATCCGTGGCCA 120
ACATCCCTATATGTAAGATTTTTTCCAAAACATGTTTCTGA 160
TTTTTAAAGTGAAAAATGCTACTTCATCATGTTCTTTTT 200
210 220 230 240
GTGCTTCTTACTTTTAAATATTAGAATGAAGAAGGAGCCCC 240
ACAGGAAGGAATTCTGGAAGATATGCCTGTGGATCCTGAC 280
AATGAGGCTTATGAAATGCCTTCTGAGGTAGGAGTCCAAG 320
CTGAATCTTTCTAACAAGACAGTACCAAAAACCTGTCATT 360
GTCACATTTCTCTTTCATTAGTGCCTTAGTGAGAATCATTT 400
410 420 430 440
GCTCTCTACATGCTCATTACGTGGACAACCTTGCAAGTTAA 440
GAATAGTTTTTACATTTTTTAAAGGGTCCTTAAAAAAAAAAG 480
AGGAGGAGGAAGATGAAGAAGAGGAAGAAAGGATGTAAAA 520
GAAATCATATGTAGTCCACATAGCTTAATATACNTACTAC 560
TTGACCTTTACAGGAAAAGCTTTACTAACCCCTGCATTA 600
610 620 630 640
GAGAATATATTTTTTTGCAAAAACATTGATTGTAAATTTT 640
AGTGTAAGTGGGGAGCCATTTCTATCTCATTGGCTGTC 680
CAGTGCTGATGCGTAATTGAAACTTATACTAACAGTGTGT 720
GCTGTCT 727

Figure 11 cont.
alpha-SYN exon 7

```

      10      20      30      40
      |      |      |      |
TTTTGATTTTCTAATATTAGGAAGGGTATCAAGACTACG 40
AACCTGAAGCCTAAGAAATATCTTTGCTCCCAGTTTCTTG 80
AGATCTGCTGACAGATGTTCCATCCTGTACAAGTGCTCAG 120
TTCCAATGTGCCCAGTCATGACATTTCTCAAAGTTTTTAC 160
AGTGTATCTCGAAGTCTTCCATCAGCAGTGATTGAAGCAT 200

      210      220      230      240
      |      |      |      |
CTGTACCTGCCCCCACTCAGCATTTCGGTGCTTCCCTTTC 240
ACTGAAGTGAATACATGGTAGCAGGGTCTTTGTGTGCTGT 280
GGATTTTGTGGCTTCAATCTACGATGTTAAAACAAATTAA 320
AAACACCTAAGTGACTACCACTTATTTCTAAATCCTCACT 360
ATTTTTTTGTGTGCTGTTGTTTCAGAAGTTGTTAGTGATTG 400

      410      420      430      440
      |      |      |      |
CTATCATATATTATNAGATTTTTAGGTGTCTTTTAATGAT 440
ACTGTCTAAGAATAATGACGTATTGTGAAATTTGTTAATA 480
TATATNATACTTAAAAATATGTGAGCATGAACTATGCAC 520
CTATAATACTAAATATGAAATTTTACCATTTTGCGATGTG 560
TTTTATTCACTTGTGTTTGTATATNAATGGTGAGAATTAA 600

      610      620      630      640
      |      |      |      |
AATAAAACGTTATCTCATTGCAAAAATATTTTATTTTAT 640
CCCATCTCACTTTAATAATAAAAAATCATGCTTATAAGCAA 680
CATGAATTAAGAACTGACACAAAGGACAAAAATATAAAGT 720
TATTAATAGCCATTTGAAGAAGGAGGAATTTTAGAAGAGG 760
TAGAGAAAAATGGAACATTAACCCTACACTCGGAATTCCT 800

      810      820      830      840
      |      |      |      |
GAAGCAACACTGCCAGAAGTGTGTTTTGGTATGCACTGGT 840
TCCTTAAGTGGCTGTGATTAATTATTGAAAGTGGGGTGTT 880
GAAGACCCCAACTACTATTGTAGAGTGGTCTATTTCTCCC 920
TTCAATCCTGTCAATGTTTGCTTTACGTATTTTGGGGAAC 960
TGTTGTTTGATGTGTATGTGTTTATAATTGTTATACATTT 1000

      1010      1020      1030      1040
      |      |      |      |
TTAATTGAGCCTTTTATTAACATATATTGTTATTTTGTG 1040
TCGAAATAATTTTTTAGTTAAAATCTATTTGTCTGATAT 1080
TGGTGTGAATGCTGTACCTTTCTGACAATAAATAATATNC 1120
GACCATGAATAAAAAAAAAAAAAAAGTGGGTTCCTGGGAA 1160
CTAAGCAGTGTAGAAGATGATTTTGACTACACCTCCTTA 1200

```


Figure 11 cont.

alpha-SYN exon 7

1210 1220 1230 1240
GAGAGCCATAAGACACATTAGCACATATTAGCACATTCAA 1240
GGCTCTGAGAGAATGTGGTTAACTTTGTTTAACTCAGCAT 1280
TCCTCACTTTTTTTTTTTAATCATCAGAAATTCTCTCTCT 1320
CTCTCTCTTTTTCTCTCGCTCTCTTTTTTTTTTTTTTTTT 1360
TTTTACAGGAAATGCCTTTAAACATCGTTGGGAAC TACCA 1400
1410 1420 1430 1440
GAGTCACCTTAAAGGGAGNATCAATTCTCTAGGACTGGAT 1440
AAAAATTTTCATGGGCCTCCTTTAAAATGTTGCCCAAATAT 1480
ATGGAATTCTAGGGGTTTTTCCNTAGGGGGAAGGGTTTTT 1520
TCTCTTTTCNGGGGAGGATCCTTTTAACNCCCCNGGGGGG 1560
NGCCCGGAAAATAAACTTGGNGGGGGGGNAAAAC TT 1596